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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=6; day=23; hr=8; min=41; sec=19; ms=406;]

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Reviewer Comments:

SEQUENCE LISTING

<110> Max-Planck-Gesellschaft zur Förderung der Wissenschaften
e.V.

Please remove the foreign accent marks in the above <110> response;
foreign accent marks are non-ASCII characters which cannot be processed.

<120> Cell line comprising vector encoding truncated FLK-1 receptor
Div. of US 09/766 678 (Pat. No. 6 872 699)

Please remove "Div. of US 09/766 678 (Pat. No. 6 872 699)" from the
above <120> response; just show the invention title. Move all prior
application data to the <150> and the <151> lines. See below:

<150> US 09/766,678

<151> 2001-01-23

The <150> is the prior application number; the <151> is the prior filing
date.

<210> 1

<211> 5470

<212> DNA

<213> Unknown

<220>

<223> SEQ ID NO: 1

The above <223> response is an insufficient explanation of "<213>

Unknown": although the <213> response is "Unknown", please try to indicate the source of the genetic material. Same type of error in Sequences 2-11.

Application No: 10799782 Version No: 2.0

Input Set:

Output Set:

Started: 2009-06-15 15:22:43.641
Finished: 2009-06-15 15:22:45.942
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 301 ms
Total Warnings: 11
Total Errors: 0
No. of SeqIDs Defined: 11
Actual SeqID Count: 11

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)

<210> 1
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<212> DNA
<213> Unknown

<220>
<223> SEQ ID NO: 1

<220>
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<222> (286)..(4386)

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acaccgctga cagccgcggc tggagccagg gcgccggtgc cccgcgctct ccccggtctt 180

gcgctgcggg ggccataacc cctctgtgac ttctttgcgg gccagggacg gagaaggagt 240

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Met Glu Ser Lys
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gcg ctg cta gct gtc gct ctg tgg ttc tgc gtg gag acc cga gcc gcc 345
Ala Leu Leu Ala Val Ala Leu Trp Phe Cys Val Glu Thr Arg Ala Ala
5 10 15 20

tct gtg ggt ttg act ggc gat ttt ctc cat ccc ccc aag ctc agc aca 393
Ser Val Gly Leu Thr Gly Asp Phe Leu His Pro Pro Lys Leu Ser Thr
25 30 35

cag aaa gac ata ctg aca att ttg gca aat aca acc ctt cag att act 441
Gln Lys Asp Ile Leu Thr Ile Leu Ala Asn Thr Thr Leu Gln Ile Thr
40 45 50

tgc agg gga cag cgg gac ctg gac tgg ctt tgg ccc aat gct cag cgt 489
Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Ala Gln Arg
55 60 65

gat tct gag gaa agg gta ttg gtg act gaa tgc ggc ggt ggt gac agt 537
Asp Ser Glu Glu Arg Val Leu Val Thr Glu Cys Gly Gly Gly Asp Ser
70 75 80

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Ile Phe Cys Lys Thr Leu Thr Ile Pro Arg Val Val Gly Asn Asp Thr
85 90 95 100

gga gcc tac aag tgc tcg tac cgg gac gtc gac ata gcc tcc act gtt 633
Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile Ala Ser Thr Val
105 110 115

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Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val Ser
120 125 130

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Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr Val	
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gtg atc ccc tgc cga ggg tcg att tca aac ctc aat gtg tct ctt tgc	777
Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn Val Ser Leu Cys	
150 155 160	
gct agg tat cca gaa aag aga ttt gtt ccg gat gga aac aga att tcc	825
Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile Ser	
165 170 175 180	
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Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr Met Ile Ser Tyr	
185 190 195	
gcc gcc atg gtc ttc tgt gag gca aag atc aat gat gaa acc tat cag	921
Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Thr Tyr Gln	
200 205 210	
tct atc atg tac ata gtt gtg gtt gta gga tat agg att tat gat gtg	969
Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr Asp Val	
215 220 225	
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Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala Gly Glu Lys Leu	
230 235 240	
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Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Leu Asp Phe	
245 250 255 260	
acc tgg cac tct cca cct tca aag tct cat cat aag aag att gta aac	1113
Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys Lys Ile Val Asn	
265 270 275	
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Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys Met Phe Leu Ser	
280 285 290	
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Thr Leu Thr Ile Glu Ser Val Thr Lys Ser Asp Gln Gly Glu Tyr Thr	
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Cys Val Ala Ser Ser Gly Arg Met Ile Lys Arg Asn Arg Thr Phe Val	
310 315 320	
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Arg Val His Thr Lys Pro Phe Ile Ala Phe Gly Ser Gly Met Lys Ser	
325 330 335 340	
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Leu Val Glu Ala Thr Val Gly Ser Gln Val Arg Ile Pro Val Lys Tyr	
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Leu Ser Tyr Pro Ala Pro Asp Ile Lys Trp Tyr Arg Asn Gly Arg Pro	
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Glu Val Thr Glu Arg Asp Ala Gly Asn Tyr Thr Val Ile Leu Thr Asn	
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Pro Ile Ser Met Glu Lys Gln Ser His Met Val Ser Leu Val Val Asn	
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Val Pro Pro Gln Ile Gly Glu Lys Ala Leu Ile Ser Pro Met Asp Ser	
425 430 435	
tac cag tat ggg acc atg cag aca ttg aca tgc aca gtc tac gcc aac	1641
Tyr Gln Tyr Gly Thr Met Gln Thr Leu Thr Cys Thr Val Tyr Ala Asn	
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cct ccc ctg cac cac atc cag tgg tac tgg cag cta gaa gaa gcc tgc	1689
Pro Pro Leu His His Ile Gln Trp Tyr Trp Gln Leu Glu Glu Ala Cys	
455 460 465	
tcc tac aga ccc ggc caa aca agc ccg tat gct tgt aaa gaa tgg aga	1737
Ser Tyr Arg Pro Gly Gln Thr Ser Pro Tyr Ala Cys Lys Glu Trp Arg	
470 475 480	
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His Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu Val Thr Lys Asn	
485 490 495 500	
caa tat gcc ctg att gaa gga aaa aac aaa act gta agt acg ctg gtc	1833
Gln Tyr Ala Leu Ile Glu Gly Lys Asn Lys Thr Val Ser Thr Leu Val	
505 510 515	
atc caa gct gcc aac gtg tca gcg ttg tac aaa tgt gaa gcc atc aac	1881
Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys Glu Ala Ile Asn	
520 525 530	
aaa gcg gga cga gga gag agg gtc atc tcc ttc cat gtg atc agg ggt	1929
Lys Ala Gly Arg Gly Glu Arg Val Ile Ser Phe His Val Ile Arg Gly	
535 540 545	
cct gaa att act gtg caa cct gct gcc cag cca act gag cag gag agt	1977
Pro Glu Ile Thr Val Gln Pro Ala Ala Gln Pro Thr Glu Gln Glu Ser	
550 555 560	
gtg tcc ctg ttg tgc act gca gac aga aat acg ttt gag aac ctc acg	2025
Val Ser Leu Leu Cys Thr Ala Asp Arg Asn Thr Phe Glu Asn Leu Thr	
565 570 575 580	
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Trp Tyr Lys Leu Gly Ser Gln Ala Thr Ser Val His Met Gly Glu Ser	
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ctc aca cca gtt tgc aag aac ttg gat gct ctt tgg aaa ctg aat ggc	2121
Leu Thr Pro Val Cys Lys Asn Leu Asp Ala Leu Trp Lys Leu Asn Gly	
600 605 610	
acc atg ttt tct aac agc aca aat gac atc ttg att gtg gca ttt cag	2169
Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile Val Ala Phe Gln	
615 620 625	
aat gcc tct ctg cag gac caa ggc gac tat gtt tgc tct gct caa gat	2217
Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys Ser Ala Gln Asp	
630 635 640	
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Lys Lys Thr Lys Lys Arg His Cys Leu Val Lys Gln Leu Ile Ile Leu	
645 650 655 660	
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Glu Arg Met Ala Pro Met Ile Thr Gly Asn Leu Glu Asn Gln Thr Thr	
665 670 675	
acc att ggc gag acc att gaa gtg act tgc cca gca tct gga aat cct	2361
Thr Ile Gly Glu Thr Ile Glu Val Thr Cys Pro Ala Ser Gly Asn Pro	
680 685 690	
acc cca cac att aca tgg ttc aaa gac aac gag acc ctg gta gaa gat	2409
Thr Pro His Ile Thr Trp Phe Lys Asp Asn Glu Thr Leu Val Glu Asp	
695 700 705	
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Ser Gly Ile Val Leu Arg Asp Gly Asn Arg Asn Leu Thr Ile Arg Arg	
710 715 720	
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Val Arg Lys Glu Asp Gly Gly Leu Tyr Thr Cys Gln Ala Cys Asn Val	
725 730 735 740	
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Leu Gly Cys Ala Arg Ala Glu Thr Leu Phe Ile Ile Glu Gly Ala Gln	
745 750 755	
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Glu Lys Thr Asn Leu Glu Val Ile Ile Leu Val Gly Thr Ala Val Ile	
760 765 770	
gcc atg ttc ttc tgg ctc ctt ctt gtc att gtc cta cgg acc gtt aag	2649
Ala Met Phe Phe Trp Leu Leu Leu Val Ile Val Leu Arg Thr Val Lys	
775 780 785	
cgg gcc aat gaa ggg gaa ctg aag aca ggc tac ttg tct att gtc atg	2697
Arg Ala Asn Glu Gly Glu Leu Lys Thr Gly Tyr Leu Ser Ile Val Met	
790 795 800	
gat cca gat gaa ttg ccc ttg gat gag cgc tgt gaa cgc ttg cct tat	2745
Asp Pro Asp Glu Leu Pro Leu Asp Glu Arg Cys Glu Arg Leu Pro Tyr	

805	810	815	820	
gat gcc agc aag tgg gaa ttc ccc agg gac cgg ctg aaa cta gga aaa				2793
Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp Arg Leu Lys Leu Gly Lys				
	825	830	835	
cct ctt ggc cgc ggt gcc ttc ggc caa gtg att gag gca gac gct ttt				2841
Pro Leu Gly Arg Gly Ala Phe Gly Gln Val Ile Glu Ala Asp Ala Phe				
	840	845	850	
gga att gac aag aca gcg act tgc aaa aca gta gcc gtc aag atg ttg				2889
Gly Ile Asp Lys Thr Ala Thr Cys Lys Thr Val Ala Val Lys Met Leu				
	855	860	865	
aaa gaa gga gca aca cac agc gag cat cga gcc ctc atg tct gaa ctc				2937
Lys Glu Gly Ala Thr His Ser Glu His Arg Ala Leu Met Ser Glu Leu				
	870	875	880	
aag atc ctc atc cac att ggt cac cat ctc aat gtg gtg aac ctc cta				2985
Lys Ile Leu Ile His Ile Gly His His Leu Asn Val Val Asn Leu Leu				
	885	890	900	
ggc gcc tgc acc aag ccg gga ggg cct ctc atg gtg att gtg gaa ttc				3033
Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu Met Val Ile Val Glu Phe				
	905	910	915	
tgc aag ttt gga aac cta tca act tac tta cgg ggc aag aga aat gaa				3081
Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu Arg Gly Lys Arg Asn Glu				
	920	925	930	
ttt gtt ccc tat aag agc aaa ggg gca cgc ttc cgc cag ggc aag gac				3129
Phe Val Pro Tyr Lys Ser Lys Gly Ala Arg Phe Arg Gln Gly Lys Asp				
	935	940	945	
tac gtt ggg gag ctc tcc gtg gat ctg aaa aga cgc ttg gac agc atc				3177
Tyr Val Gly Glu Leu Ser Val Asp Leu Lys Arg Arg Leu Asp Ser Ile				
	950	955	960	
acc agc agc cag agc tct gcc agc tca ggc ttt gtt gag gag aaa tcg				3225
Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly Phe Val Glu Glu Lys Ser				
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ctc agt gat gta gag gaa gaa gaa gct tct gaa gaa ctg tac aag gac				3273
Leu Ser Asp Val Glu Glu Glu Glu Ala Ser Glu Glu Leu Tyr Lys Asp				
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ttc ctg acc ttg gag cat ctc atc tgt tac agc ttc caa gtg gct				3318
Phe Leu Thr Leu Glu His Leu Ile Cys Tyr Ser Phe Gln Val Ala				
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Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp				
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Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn Val Val Lys				
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Tyr Val Arg Lys	Gly Asp Ala Arg Leu	Pro Leu Lys Trp Met Ala	
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ccg gaa acc att	ttt gac aga gta tac	aca att cag agc gat gtg	3543
Pro Glu Thr Ile	Phe Asp Arg Val Tyr	Thr Ile Gln Ser Asp Val	
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Trp Ser Phe Gly	Val Leu Leu Trp Glu	Ile Phe Ser Leu Gly Ala	
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Leu Gln Ala Asn	Ala Gln Gln Asp Gly	Lys Asp Tyr Ile Val Leu	
1165	1170	1175	
cca atg tca gag	aca ctg agc atg gaa	gag gat tct gga ctc tcc	3858
Pro Met Ser Glu	Thr Leu Ser Met Glu	Glu Asp Ser Gly Leu Ser	
1180			